RAW SEQUENCE LISTING

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Application Serial Number: 10|619,992

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RAW SEQUENCE LISTING   DATE: 06/22/2005
PATENT APPLICATION: **US/10/619,992**   TIME: 09:19:38

Input Set : **N:\Crf3\RULE60\10619992.raw**
Output Set: **N:\CRF4\06222005\J619992.raw**

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 1 <110> APPLICANT: Hefeneider, Steven
 2         Merkins, Louise
 3         Bennett, Robert
 4         Seiss, Donald
 5 <120> TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding
Gene and Uses
 6 <130> FILE REFERENCE: 00-617-A
 7 <140> CURRENT APPLICATION NUMBER: US/10/619,992
 8 <141> CURRENT FILING DATE: 2003-07-15
 9 <150> PRIOR APPLICATION NUMBER: US/09/921,099
10 <151> PRIOR FILING DATE: 2001-08-01
11 <160> NUMBER OF SEQ ID NOS: 21
12 <170> SOFTWARE: PatentIn version 3.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 4351
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (602)..(4174)
21 <400> SEQUENCE: 1
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24         tattatgttt tggggtactg gttatccaag ggaaacactt ttttaaacaa caaaacaaaa     180
25         aaaccgccca gcagtccaaa gtaatttgtg ttcctaaaaa tggaatatgg aaagttaatt     240
26         tgcttgtttg atgtggtcgt tgagaaaaat acataaaagc tttgatgttt attatgtgag     300
27         caaccaatat aaatacagtt tagttgaaag gaacactatt aaggtattgt ttccaggcag     360
28         aatttcagaa atgtaattaa ttcagcaaat aggttttta aaaagacat ccaaaggtta     420
29         taaaattatt tagaagtatt ttaggtctga agctgtaata gttgacttaa gcaattaact     480
30         cttcaaaggt gaatgatgaa tatgtggtta attcatactt ttgtccattt ctagcttaca     540
31         aaacactaca cagcaaaata atgatctgct agactgctaa cccgagcatc cagcttccac     600
32         a atg cct gtg cag gca gct caa tgg aca gaa ttt ctg tcc tgt cca atc     649
33           Met Pro Val Gln Ala Ala Gln Trp Thr Glu Phe Leu Ser Cys Pro Ile
34           1               5                  10                  15
35         tgc tat aat gaa ttt gat gag aat gtg cac aaa ccc atc agt tta ggt     697
36         Cys Tyr Asn Glu Phe Asp Glu Asn Val His Lys Pro Ile Ser Leu Gly
37                         20                  25                  30
38         tgt tca cac act gtt tgc aag acc tgc ttg aat aaa ctt cat cga aaa     745
39         Cys Ser His Thr Val Cys Lys Thr Cys Leu Asn Lys Leu His Arg Lys
40                 35                  40                  45
41         gct tgt cct ttt gac cag act gcc atc aac aca gat att gat gta ctt     793
42         Ala Cys Pro Phe Asp Gln Thr Ala Ile Asn Thr Asp Ile Asp Val Leu
43             50                  55                  60
44         cct gtc aac ttc gca ctt ctc cag tta gtt gga gcc cag gta cca gat     841
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45    Pro Val Asn Phe Ala Leu Leu Gln Leu Val Gly Ala Gln Val Pro Asp
46    65                      70                  75                  80
47    cat cag tca att aag tta agt aat cta ggt gag aat aaa cac tat gag      889
48    His Gln Ser Ile Lys Leu Ser Asn Leu Gly Glu Asn Lys His Tyr Glu
49                        85                  90                  95
50    gtt gca aag aaa tgc gtt gag gat ttg gca ctc tac tta aaa cca cta      937
51    Val Ala Lys Lys Cys Val Glu Asp Leu Ala Leu Tyr Leu Lys Pro Leu
52                        100                 105                 110
53    agt gga ggt aaa ggt gta gct agc ttg aac cag agt gca ctg agc cgt      985
54    Ser Gly Gly Lys Gly Val Ala Ser Leu Asn Gln Ser Ala Leu Ser Arg
55                        115                 120                 125
56    cca atg caa agg aaa ctg gtg aca ctt gta aac tgt caa ctg gtg gag     1033
57    Pro Met Gln Arg Lys Leu Val Thr Leu Val Asn Cys Gln Leu Val Glu
58                130                 135                 140
59    gaa gaa ggt cgt gta aga gcc atg cga gca gct cgt tcc ctt gga gaa     1081
60    Glu Glu Gly Arg Val Arg Ala Met Arg Ala Ala Arg Ser Leu Gly Glu
61    145                 150                 155                 160
62    aga act gta aca gaa ctg ata tta cag cac cag aac cct cag cag ttg     1129
63    Arg Thr Val Thr Glu Leu Ile Leu Gln His Gln Asn Pro Gln Gln Leu
64                        165                 170                 175
65    tct gcc aat cta tgg gcc gct gtc agg gct cga gga tgc cag ttt tta     1177
66    Ser Ala Asn Leu Trp Ala Ala Val Arg Ala Arg Gly Cys Gln Phe Leu
67                        180                 185                 190
68    ggg cca gct atg caa gaa gag gcc ttg aag ctg gtg tta ctg gca tta     1225
69    Gly Pro Ala Met Gln Glu Glu Ala Leu Lys Leu Val Leu Leu Ala Leu
70                        195                 200                 205
71    gaa gat ggt tct gcc ctc tca agg aaa gtt ctg gta ctt ttt gtt gtg     1273
72    Glu Asp Gly Ser Ala Leu Ser Arg Lys Val Leu Val Leu Phe Val Val
73                210                 215                 220
74    cag aga cta gaa cca aga ttt cct cag gca tca aaa aca agt att ggt     1321
75    Gln Arg Leu Glu Pro Arg Phe Pro Gln Ala Ser Lys Thr Ser Ile Gly
76    225                 230                 235                 240
77    cat gtt gtg caa cta ctg tat cga gct tct tgt ttt aag gtt acc aaa     1369
78    His Val Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Lys Val Thr Lys
79                        245                 250                 255
80    aga gat gaa gac tct tcc cta atg cag ctg aag gag gaa ttt cgg agt     1417
81    Arg Asp Glu Asp Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Ser
82                260                 265                 270
83    tat gaa gca tta cgc aga gaa cat gat gcc caa att gtt cat att gcc     1465
84    Tyr Glu Ala Leu Arg Arg Glu His Asp Ala Gln Ile Val His Ile Ala
85                275                 280                 285
86    atg gaa gca gga ctc cgt att tca cct gaa cag tgg tcc tct ctt ttg     1513
87    Met Glu Ala Gly Leu Arg Ile Ser Pro Glu Gln Trp Ser Ser Leu Leu
88                290                 295                 300
89    tat ggt gat ttg gct cat aaa tca cac atg cag tct atc att gat aag     1561
90    Tyr Gly Asp Leu Ala His Lys Ser His Met Gln Ser Ile Ile Asp Lys
91    305                 310                 315                 320
92    cta cag tct cca gag tca ttt gca aag agt gtc cag gaa ttg aca att     1609
93    Leu Gln Ser Pro Glu Ser Phe Ala Lys Ser Val Gln Glu Leu Thr Ile
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Input Set : **N:\Crf3\RULE60\10619992.raw**
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 94                  325                 330                 335
 95    gtt ttg caa cga aca ggt gac cca gct aac tta aat aga ctg agg cct    1657
 96    Val Leu Gln Arg Thr Gly Asp Pro Ala Asn Leu Asn Arg Leu Arg Pro
 97                  340                 345                 350
 98    cat tta gag ctt ctt gca aac ata gac cct aat cca gac gct gtt tca    1705
 99    His Leu Glu Leu Leu Ala Asn Ile Asp Pro Asn Pro Asp Ala Val Ser
100                  355                 360                 365
101    cca act tgg gag cag ctg gaa aat gca atg gta gct gtt aaa aca gta    1753
102    Pro Thr Trp Glu Gln Leu Glu Asn Ala Met Val Ala Val Lys Thr Val
103                  370                 375                 380
104    gtt cat ggc ctt gtg gac ttc ata caa aat tat agt aga aaa ggc cat    1801
105    Val His Gly Leu Val Asp Phe Ile Gln Asn Tyr Ser Arg Lys Gly His
106    385                  390                 395                 400
107    gag acc cct cag cct cag cca aac agc aaa tac aag act agc atg tgc    1849
108    Glu Thr Pro Gln Pro Gln Pro Asn Ser Lys Tyr Lys Thr Ser Met Cys
109                  405                 410                 415
110    cga gat ttg cga cag cag ggg ggt tgt cca cga gga aca aat tgt aca    1897
111    Arg Asp Leu Arg Gln Gln Gly Gly Cys Pro Arg Gly Thr Asn Cys Thr
112                  420                 425                 430
113    ttt gcc cat tct cag gaa gag ctt gaa aag tat cga tta agg aac aaa    1945
114    Phe Ala His Ser Gln Glu Glu Leu Glu Lys Tyr Arg Leu Arg Asn Lys
115                  435                 440                 445
116    aag atc aat gcc act gta aga acg ttt cct ctt cta aat aaa gtt ggt    1993
117    Lys Ile Asn Ala Thr Val Arg Thr Phe Pro Leu Leu Asn Lys Val Gly
118                  450                 455                 460
119    gta aac aac act gtc aca acc aca gcc gga aat gtc att tct gtc ata    2041
120    Val Asn Asn Thr Val Thr Thr Thr Ala Gly Asn Val Ile Ser Val Ile
121    465                  470                 475                 480
122    gga agt act gaa aca aca ggg aaa att gtt cca agt aca aac gga att    2089
123    Gly Ser Thr Glu Thr Thr Gly Lys Ile Val Pro Ser Thr Asn Gly Ile
124                  485                 490                 495
125    tca aat gca gaa aac agt gtt tcc cag cta atc tca cgt agt act gac    2137
126    Ser Asn Ala Glu Asn Ser Val Ser Gln Leu Ile Ser Arg Ser Thr Asp
127                  500                 505                 510
128    agt acc tta aga gct ctg gag acc gtg aag aaa gtg gga aag gtt ggc    2185
129    Ser Thr Leu Arg Ala Leu Glu Thr Val Lys Lys Val Gly Lys Val Gly
130                  515                 520                 525
131    gct aat ggt cag aat gct gct ggg ccc tct gca gat tct gta act gaa    2233
132    Ala Asn Gly Gln Asn Ala Ala Gly Pro Ser Ala Asp Ser Val Thr Glu
133                  530                 535                 540
134    aat aaa att ggt tct cca ccc aag act cct gta agt aat gta gca gct    2281
135    Asn Lys Ile Gly Ser Pro Pro Lys Thr Pro Val Ser Asn Val Ala Ala
136    545                  550                 555                 560
137    acc tca gct ggg ccc tct aat gtt gga aca gag ctg aat tct gtg cct    2329
138    Thr Ser Ala Gly Pro Ser Asn Val Gly Thr Glu Leu Asn Ser Val Pro
139                  565                 570                 575
140    caa aaa tcc agc cca ttt cta act aga gta cca gta tat cct ccg cat    2377
141    Gln Lys Ser Ser Pro Phe Leu Thr Arg Val Pro Val Tyr Pro Pro His
142                  580                 585                 590
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143   tct gaa aac att cag tat ttt caa gat cca agg act cag ata ccc ttt   2425
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145           595                 600                 605
146   gaa gtc cca cag tac cca cag aca gga tac tat cca cca cct cca acg   2473
147   Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr
148           610                 615                 620
149   gta cca gct ggt gtg gct ccc tgt gtt cct cgc ttt gtg agg tcc aat   2521
150   Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn
151   625                 630                 635                 640
152   aac gtt cca gag tcc tcc ctc cca cct gct tcc atg cca tat gcc gat   2569
153   Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp
154           645                 650                 655
155   cat tac agt aca ttt tcc cct cga gat cga atg aat tct tct cct tac   2617
156   His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr
157           660                 665                 670
158   cag cct cct cct ccg cag ccg tat gga cca gtt cct cca gta cct tct   2665
159   Gln Pro Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser
160           675                 680                 685
161   gga atg tat gct cct gtg tac gac agc agg cgc atc tgg cgc cca cct   2713
162   Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro
163           690                 695                 700
164   atg tac caa cga gat gac att att aga agc aat tct tta cct cca atg   2761
165   Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met
166   705                 710                 715                 720
167   gat gtg atg cac tca tct gtc tat cag aca tct ttg cgg gaa aga tat   2809
168   Asp Val Met His Ser Ser Val Tyr Gln Thr Ser Leu Arg Glu Arg Tyr
169           725                 730                 735
170   aac tca tta gat gga tat tat tcg gtg gct tgt cag cca cca agt gag   2857
171   Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu
172           740                 745                 750
173   cca agg aca act gtg cct tta cca agg gaa cct tgt ggt cat ttg aag   2905
174   Pro Arg Thr Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys
175           755                 760                 765
176   acc agt tgc gag gag cag ata aga aga aag cca gat cag tgg gca cag   2953
177   Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln
178           770                 775                 780
179   tac cac act cag aaa gca cct ctt gtc tct tca act ctt cct gtg gca   3001
180   Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala
181   785                 790                 795                 800
182   aca cag tca cca aca cca cct tct cct ctg ttc agt gta gac ttt cgt   3049
183   Thr Gln Ser Pro Thr Pro Pro Ser Pro Leu Phe Ser Val Asp Phe Arg
184           805                 810                 815
185   gcg gat ttc tca gag agt gtg agt ggt aca aaa ttt gaa gaa gat cat   3097
186   Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His
187           820                 825                 830
188   ctt tcc cat tat tct ccc tgg tct tgt ggc acc ata ggc tcc tgt ata   3145
189   Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile
190           835                 840                 845
191   aat gcc att gat tca gag ccc aaa gat gtc att gct aat tca aat gct   3193
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192    Asn Ala Ile Asp Ser Glu Pro Lys Asp Val Ile Ala Asn Ser Asn Ala
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194    gtg tta atg gac ctg gac agt ggt gat gtt aag aga aga gta cat tta    3241
195    Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu
196    865                   870               875               880
197    ttt gaa acc cag aga agg aca aaa gaa gaa gat cca ata att ccc ttt    3289
198    Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe
199                      885               890               895
200    agt gat gga ccc atc atc tca aaa tgg ggt gcg att tcc aga tct tcc    3337
201    Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser
202                  900               905               910
203    cgt aca ggt tac cat acc aca gat cct gtc cag gcc act gct tcc caa    3385
204    Arg Thr Gly Tyr His Thr Thr Asp Pro Val Gln Ala Thr Ala Ser Gln
205              915               920               925
206    gga agt gcg act aag ccc atc agt gta tca gat tat gtc cct tat gtc    3433
207    Gly Ser Ala Thr Lys Pro Ile Ser Val Ser Asp Tyr Val Pro Tyr Val
208         930               935               940
209    aat gct gtt gat tca agg tgg agt tca tat ggc aac gag gcc aca tca    3481
210    Asn Ala Val Asp Ser Arg Trp Ser Ser Tyr Gly Asn Glu Ala Thr Ser
211    945               950               955               960
212    tca gca cac tat gtt gaa agg gac aga ttc att gtt act gat tta tct    3529
213    Ser Ala His Tyr Val Glu Arg Asp Arg Phe Ile Val Thr Asp Leu Ser
214                  965               970               975
215    ggt cat aga aag cat tcc agt act ggg gac ctt ttg agc ctt gaa ctt    3577
216    Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu
217                  980               985               990
218    cag cag gcc aag agc aac tca tta  ctt ctt cag aga gag  gcc aat gct    3625
219    Gln Gln Ala Lys Ser Asn Ser Leu  Leu Leu Gln Arg Glu  Ala Asn Ala
220              995               1000              1005
221    ttg gcc  atg caa cag aag tgg  aat tcc ctg gat gaa  ggc cgt cac    3670
222    Leu Ala  Met Gln Gln Lys Trp  Asn Ser Leu Asp Glu  Gly Arg His
223         1010              1015              1020
224    ctt acc  tta aac ctt tta agc  aag gaa att gaa cta  aga aat gga    3715
225    Leu Thr  Leu Asn Leu Leu Ser  Lys Glu Ile Glu Leu  Arg Asn Gly
226         1025              1030              1035
227    gag tta  cag agt gat tat aca  gaa gat gca aca gat  act aaa cct    3760
228    Glu Leu  Gln Ser Asp Tyr Thr  Glu Asp Ala Thr Asp  Thr Lys Pro
229         1040              1045              1050
230    gat agg  gat atc gag tta gag  ctt tca gca ctt gat  act gat gaa    3805
231    Asp Arg  Asp Ile Glu Leu Glu  Leu Ser Ala Leu Asp  Thr Asp Glu
232         1055              1060              1065
233    cct gat  gga caa agt gaa cca  att gaa gag atc ttg  gac ata cag    3850
234    Pro Asp  Gly Gln Ser Glu Pro  Ile Glu Glu Ile Leu  Asp Ile Gln
235         1070              1075              1080
236    ctt ggt  atc agt tct caa aat  gat cag ttg cta aat  gga atg gca    3895
237    Leu Gly  Ile Ser Ser Gln Asn  Asp Gln Leu Leu Asn  Gly Met Ala
238         1085              1090              1095
239    gtg gaa  aat ggg cat cca gta  cag cag cac caa aag  gag cca cca    3940
240    Val Glu  Asn Gly His Pro Val  Gln Gln His Gln Lys  Glu Pro Pro
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<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6

VERIFICATION SUMMARY   DATE: 06/22/2005
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